



PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/807,132

DATE: 09/18/2002

TIME: 15:42:32

Input Set : A:\06501-075001.TXT

Output Set: N:\CRF4\09182002\I807132.raw

pb

ENTERED

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4 <110> APPLICANT: Maeda, Masatsugu
5     Nakata, Yasuhiko
6     Nomura, Hitoshi
8 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
10 <130> FILE REFERENCE: 06501-075001
12 <140> CURRENT APPLICATION NUMBER: US 09/807,132
13 <141> CURRENT FILING DATE: 2001-04-06
15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05578
16 <151> PRIOR FILING DATE: 1999-10-08
18 <150> PRIOR APPLICATION NUMBER: JP 10/288565
19 <151> PRIOR FILING DATE: 1998-10-09
21 <150> PRIOR APPLICATION NUMBER: JP 10/347546
22 <151> PRIOR FILING DATE: 1998-12-07
24 <150> PRIOR APPLICATION NUMBER: JP 10/363537
25 <151> PRIOR FILING DATE: 1998-12-21
27 <160> NUMBER OF SEQ ID NOS: 62
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 1143
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
36 <220> FEATURE:
37 <221> NAME/KEY: CDS
38 <222> LOCATION: (9)...(947)
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41 ctcatgga atg gac agt cta aac caa aca aga gtg act gaa ttt gtc ttc      50
42     Met Asp Ser Leu Asn Gln Thr Arg Val Thr Glu Phe Val Phe
43         1             5             10
45 ttg gga ctc act gat aac cgg gtg ctg gaa atg ctg ttt ttc atg gca      98
46 Leu Gly Leu Thr Asp Asn Arg Val Leu Glu Met Leu Phe Phe Met Ala
47 15             20             25             30
49 ttc tca gcc att tat atg cta acg ctt tca ggg aac att ctc atc atc      146
50 Phe Ser Ala Ile Tyr Met Leu Thr Leu Ser Gly Asn Ile Leu Ile Ile
51         35             40             45
53 att gcc aca gtc ttt act cca agt ctc cat acc ccc atg tat ttc ttc      194
54 Ile Ala Thr Val Phe Thr Pro Ser Leu His Thr Pro Met Tyr Phe Phe
55         50             55             60
57 ctg agc aat ctg tcc ttt att gac atc tgc cac tca tct gtc act gtg      242
58 Leu Ser Asn Leu Ser Phe Ile Asp Ile Cys His Ser Ser Val Thr Val
59         65             70             75
61 cct aag atg ttg gag ggt ttg ctt tta gaa aga aag acc att tcc ttt      290
62 Pro Lys Met Leu Glu Gly Leu Leu Leu Glu Arg Lys Thr Ile Ser Phe
63         80             85             90

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65 gac aac tgc atc aca cag ctc ttc ttc cta cat ctc ttt gcc tgt gcc      338
66 Asp Asn Cys Ile Thr Gln Leu Phe Phe Leu His Leu Phe Ala Cys Ala
67 95      100      105      110
69 gag atc ttt ctg ctg atc att gtg gcg tat gat cgt tac gtg gct atc      386
70 Glu Ile Phe Leu Leu Ile Ile Val Ala Tyr Asp Arg Tyr Val Ala Ile
71      115      120      125
73 tgc act cca ctc cac tac ccc aat gtg atg aac atg aga gtc tgt ata      434
74 Cys Thr Pro Leu His Tyr Pro Asn Val Met Asn Met Arg Val Cys Ile
75      130      135      140
77 cag ctt gtc ttt gct ctc tgg ttg ggg ggt act gtt cac tca cta ggg      482
78 Gln Leu Val Phe Ala Leu Trp Leu Gly Gly Thr Val His Ser Leu Gly
79      145      150      155
81 cag acc ttc ttg act att cgt cta cct tac tgt ggc ccc aac att att      530
82 Gln Thr Phe Leu Thr Ile Arg Leu Pro Tyr Cys Gly Pro Asn Ile Ile
83      160      165      170
85 gac agc tac ttc tgt gat gtg cct ctt gtt atc aag ctg gcc tgc aca      578
86 Asp Ser Tyr Phe Cys Asp Val Pro Leu Val Ile Lys Leu Ala Cys Thr
87 175      180      185      190
89 gat aca tac ctc aca gga ata ctg att gtg acc aat agt gga acc atc      626
90 Asp Thr Tyr Leu Thr Gly Ile Leu Ile Val Thr Asn Ser Gly Thr Ile
91      195      200      205
93 tcc ctc tcc tgt ttc ttg gcc gtg gtc acc tcc tat atg gtc atc ctg      674
94 Ser Leu Ser Cys Phe Leu Ala Val Val Thr Ser Tyr Met Val Ile Leu
95      210      215      220
97 gtt tct ctt cga aaa cac tca gct gaa ggg cgc cag aaa gcc ctg tct      722
98 Val Ser Leu Arg Lys His Ser Ala Glu Gly Arg Gln Lys Ala Leu Ser
99      225      230      235
101 acc tgc tgc gcc cac ttc atg gtg gtt gcc ctc ttc ttt ggg cca tgt      770
102 Thr Cys Ser Ala His Phe Met Val Val Ala Leu Phe Phe Gly Pro Cys
103      240      245      250
105 atc ttc atc tat act cgg cca gac acc agc ttc tcc att gac aag gtg      818
106 Ile Phe Ile Tyr Thr Arg Pro Asp Thr Ser Phe Ser Ile Asp Lys Val
107 255      260      265      270
109 gtg tct gtc ttc tac aca gtg gtc acc cct ttg ctg aat ccc ttc att      866
110 Val Ser Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Phe Ile
111      275      280      285
113 tac acc ttg agg aat gag gag gta aaa agt gcc atg aag cag ctc agg      914
114 Tyr Thr Leu Arg Asn Glu Glu Val Lys Ser Ala Met Lys Gln Leu Arg
115      290      295      300
117 cag aga caa gtt ttt ttc acg aaa tca tat aca taatgggcat tgggattgca      967
118 Gln Arg Gln Val Phe Phe Thr Lys Ser Tyr Thr
119      305      310
121 gacataattg cagccacatc cttaatgaaa gagcaaaagt aaagagtcaa aatcaactta      1027
122 tataacttgg taaattaggt aaaatggcat agagcaggtc agatttctgc tcattaaaga      1087
123 taagaactta ttctgttcac taaagataag aacttattaa ctattattta aataaa      1143
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 1248
127 <212> TYPE: DNA
128 <213> ORGANISM: Homo sapiens

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130 &lt;220&gt; FEATURE:

131 &lt;221&gt; NAME/KEY: CDS

132 &lt;222&gt; LOCATION: (13)...(951)

134 &lt;400&gt; SEQUENCE: 2

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135 attctctgagg at atg gaa aga atc aac agc aca ctg ttg act gcg ttt atc      51
136           Met Glu Arg Ile Asn Ser Thr Leu Leu Thr Ala Phe Ile
137           1           5           10
139 ctg aca gga att ccg tat cca ctc agg cta agg aca ctc ttt ttt gtg      99
140 Leu Thr Gly Ile Pro Tyr Pro Leu Arg Leu Arg Thr Leu Phe Phe Val
141           15           20           25
143 ttc ttt ttt cta atc tac atc ctg act cag ctg gga aac ctg ctt att      147
144 Phe Phe Phe Leu Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile
145           30           35           40           45
147 tta atc act gtc tgg gca gac cca agg ctc cat gcc cgc ccc atg tac      195
148 Leu Ile Thr Val Trp Ala Asp Pro Arg Leu His Ala Arg Pro Met Tyr
149           50           55           60
151 atc ttt ctt ggt gtt ctc tca gtc att gat atg agc atc tcc tcc atc      243
152 Ile Phe Leu Gly Val Leu Ser Val Ile Asp Met Ser Ile Ser Ser Ile
153           65           70           75
155 att gtc cct cgc ctc atg atg aac ttc act tta ggt gtc aaa ccc atc      291
156 Ile Val Pro Arg Leu Met Met Asn Phe Thr Leu Gly Val Lys Pro Ile
157           80           85           90
159 cca ttt ggt ggc tgt gtt gct caa ctc tat ttc tat cac ttc ctg ggc      339
160 Pro Phe Gly Gly Cys Val Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly
161           95           100           105
163 agc acc cag tgc ttc ctc tac acc cta atg gcc tat gac agg tac ctg      387
164 Ser Thr Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu
165           110           115           120           125
167 gca ata tgt cag ccc ctg cgc tac cct gtg ctc atg act gct aag ctg      435
168 Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Thr Ala Lys Leu
169           130           135           140
171 agc gcc ttg ctt gtg gct gga gcc tgg atg gca gga tcc atc cat ggg      483
172 Ser Ala Leu Leu Val Ala Gly Ala Trp Met Ala Gly Ser Ile His Gly
173           145           150           155
175 gct ctc cag gcc atc cta acc ttc cgc ctg ccc tac tgt ggg ccc aat      531
176 Ala Leu Gln Ala Ile Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn
177           160           165           170
179 cag gtg gat tac ttc ttc tgt gac atc cct gca gtg ttg aga ctg gcc      579
180 Gln Val Asp Tyr Phe Phe Cys Asp Ile Pro Ala Val Leu Arg Leu Ala
181           175           180           185
183 tgt gct gac aca aca gtc aac gag ctg gtg acg ttt gta gac att ggg      627
184 Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile Gly
185           190           195           200           205
187 gtg gtg gtt gcc agt tgc ttc tcc ctg atc ctc ctc tcc tac ata cag      675
188 Val Val Val Ala Ser Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln
189           210           215           220
191 atc att cag gcc atc ctg aga atc cac aca gct gat ggg cgg cgc cgg      723
192 Ile Ile Gln Ala Ile Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg
193           225           230           235

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195 gct ttt tca act tgt gga gcc cat gta acc gtg gtc acc gtg tac tat      771
196 Ala Phe Ser Thr Cys Gly Ala His Val Thr Val Val Thr Val Tyr Tyr
197          240          245          250
199 gtg ccc tgt gcc ttc atc tac ctg agg cct gaa acc aac agc ccc ctg      819
200 Val Pro Cys Ala Phe Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu
201          255          260          265
203 gat ggg gca gct gcc cta gtc ccc acg gcc atc act cct ttc ctc aac      867
204 Asp Gly Ala Ala Ala Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn
205 270          275          280          285
207 ccc ctt atc tac act ctg cgg aac caa gag gtg aag ctg gcc ctg aaa      915
208 Pro Leu Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys
209          290          295          300
211 aga atg ctc aga agc cca aga act ccg agt gag gtt tgaaagtgtc      961
212 Arg Met Leu Arg Ser Pro Arg Thr Pro Ser Glu Val
213          305          310
215 tttctccac tagggaagct gccacaatta gaatttatta taatgttttag gcttcggtaa 1021
216 cttttttctt ttcttcttgt tttttctctt ttatatagcc atactgtatg atcaaacaca 1081
217 gtttaaggta aaatactaac tttctaacag ttccttagta tcctctcaag ataactctca 1141
218 gccactgcaa gagtagagaa tgagacaaaa ttctcacaaa ctaaaccaca ttaaacaatc 1201
219 cagaagaaag aatgcaatag tgtattttcc aatgtctcag taataaa      1248
221 <210> SEQ ID NO: 3
222 <211> LENGTH: 1431
223 <212> TYPE: DNA
224 <213> ORGANISM: Homo sapiens
226 <220> FEATURE:
227 <221> NAME/KEY: CDS
228 <222> LOCATION: (410)...(1339)
230 <400> SEQUENCE: 3
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232 tcgctctgtt gccagagctg gagtgtagtg gcgccatctc ggctcgctgc ggtctccgcc      120
233 tcccgggttc aggcgattct ccggcctcag cctcccgggt gcgtgggatt gcaggaacta      180
234 gaactaaagc gaggttaatt tccacagtga gaacatgtc cagacatccg agcaccagtg      240
235 tggtcttgga aactccacag ataccacagg actagaaaat aactggacaa tgggatgttc      300
236 tatcttgccc gaactgaggg atataaaaag ctccaaagac aaagaaagta ccatccaccc      360
237 atcccaaaaag aaattatcct tccttctgaa aataagactg caaaaagac atg gga aag      418
238                                     Met Gly Lys
239                                     1
241 acc aaa aac aca tcg ctg gat gcc gtg gtg aca gat ttc att ctt ctg      466
242 Thr Lys Asn Thr Ser Leu Asp Ala Val Val Thr Asp Phe Ile Leu Leu
243          5          10          15
245 ggt ttg tct cac ccc cca aat cta aga agc ctc ctc ttc ctg gtc ttc      514
246 Gly Leu Ser His Pro Pro Asn Leu Arg Ser Leu Leu Phe Leu Val Phe
247 20          25          30          35
249 ttc atc att tac atc ctc act cag ctg ggg aac ctg ctc att ctg ctc      562
250 Phe Ile Ile Tyr Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Leu
251          40          45          50
253 acc atg tgg gct gac ccg aag ctc tgt gct cgc ccc atg tac att ctt      610
254 Thr Met Trp Ala Asp Pro Lys Leu Cys Ala Arg Pro Met Tyr Ile Leu
255          55          60          65

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257 ctg gga gtg ctc tca ttc ctg gac atg tgg ctc tcc tca gtc acc gtt      658
258 Leu Gly Val Leu Ser Phe Leu Asp Met Trp Leu Ser Ser Val Thr Val
259      70      75      80
261 cct cgg ctt att ttg gat ttt act cct tcc atc aag gct atc ccg ttt      706
262 Pro Arg Leu Ile Leu Asp Phe Thr Pro Ser Ile Lys Ala Ile Pro Phe
263      85      90      95
265 ggt ggc tgt gtg gct caa ctg tat ttc ttt cac ttc ctg ggc agc acc      754
266 Gly Gly Cys Val Ala Gln Leu Tyr Phe Phe His Phe Leu Gly Ser Thr
267 100      105      110      115
269 cag tgc ttc ctc tac acc ttg atg gcc tat gac agg tac cta gca ata      802
270 Gln Cys Phe Leu Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile
271      120      125      130
273 tgt cag ccc ctg cac tac cca gtg ctc atg aat ggg agg tta tgc aca      850
274 Cys Gln Pro Leu His Tyr Pro Val Leu Met Asn Gly Arg Leu Cys Thr
275      135      140      145
277 gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc atg cat ggg tct atc      898
278 Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Met His Gly Ser Ile
279      150      155      160
281 cag gcc acc ttg acc ttc cgc ctg ccc tac tgt ggg ccc aat cag gtg      946
282 Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val
283      165      170      175
285 gat tac ttt atc tgt gac atc cgc gca gta ttg aga ctg gcc tgt gct      994
286 Asp Tyr Phe Ile Cys Asp Ile Arg Ala Val Leu Arg Leu Ala Cys Ala
287 180      185      190      195
289 gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc agg gta gtg      1042
290 Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val Arg Val Val
291      200      205      210
293 gcc gcc agt tgc ttc atg tta att ctg ctc tcc tat gcc aac ata gtc      1090
294 Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala Asn Ile Val
295      215      220      225
297 cat gcc atc ctg aag ata cgc acc gct gat ggg agg cgc cgg gcc ttc      1138
298 His Ala Ile Leu Lys Ile Arg Thr Ala Asp Gly Arg Arg Arg Ala Phe
299      230      235      240
301 tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac tat gtc ccc      1186
302 Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr Tyr Val Pro
303      245      250      255
305 tgt att ttc atc tac ctt agg gct ggc tcc aaa gac ccc ctg gat ggg      1234
306 Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Asp Pro Leu Asp Gly
307 260      265      270      275
309 gca gcg gct gtg ttt tac act gtt gtc act cca tta ctg aac ccc ctc      1282
310 Ala Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu Asn Pro Leu
311      280      285      290
313 atc tat aca ctg agg aac cag gaa gtg aag tct gcc ctg aag agg ata      1330
314 Ile Tyr Thr Leu Arg Asn Gln Glu Val Lys Ser Ala Leu Lys Arg Ile
315      295      300      305
317 aca gca ggt tgaaggactg aatgaaaata agtaactaca tctgcatcat      1379
318 Thr Ala Gly
319      310
321 tatcactgcc actctcttca gctactgctg catgtgacaa atgcccataa aa      1431

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:54; Xaa Pos. 7,9